

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: March 17, 2003, 16:35:11 ; Search time 10 Seconds

(without alignments)  
1078.385 Million cell updates/sec

Title: US-09-840-243B-11

Perfect score: 1341

Sequence: 1 MELTQPAEDLIQTQTPASE.....VIENHILKLFQSNLVPADPE 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1341	100.0	260	1 RFXK_HUMAN	Q14593 homo sapien
2	1113.5	83.0	269	1 RFXK_MOUSE	Q92205 mus musculu
3	202.5	15.1	3924	1 ANK2_HUMAN	Q01484 homo sapien
4	193	14.4	4377	1 ANK3_HUMAN	Q12955 homo sapien
5	187	13.9	1327	1 TNK1_HUMAN	Q95271 homo sapien
6	184	13.7	1880	1 ANK1_HUMAN	P16157 homo sapien
7	183	13.6	1862	1 ANK1_MOUSE	Q02357 mus musculu
8	182.5	13.6	231	1 PSDA_MOUSE	Q922x2 mus musculu
9	181.5	13.5	768	1 YB23_HUMAN	Q9ulj7 homo sapien
10	176.5	13.2	226	1 PSDA_HUMAN	Q75832 homo sapien
11	176.5	13.2	231	1 PSDA_RAT	Q922x3 rattus norv
12	175	13.0	328	1 ANR2_MOUSE	Q9wv06 mus musculu
13	173	12.9	333	1 ANR2_HUMAN	Q9gzv1 homo sapien
14	172.5	12.9	1059	1 Y379_HUMAN	Q15084 homo sapien
15	169.5	12.6	451	1 ILK_CAVPO	P57044 cavia porce
16	169.5	12.6	741	1 RNSA_HUMAN	Q05823 homo sapien
17	168	12.5	776	1 ANR5_HUMAN	Q9nu02 homo sapien
18	165.5	12.3	452	1 ILK1_HUMAN	Q13418 homo sapien
19	165.5	12.3	452	1 ILK2_HUMAN	P57043 homo sapien
20	164	12.2	642	1 YAZA_SCHPO	Q09701 schizosacch
21	163.5	12.2	518	1 ASB3_HUMAN	Q9y575 homo sapien
22	163	12.2	117	1 MTN_HUMAN	P80144 mus musculu
23	163	12.2	118	1 MTN_MOUSE	Q91955 gallus gall
24	163	12.2	439	1 AKR_ARATH	Q05753 arabidopsis
25	163	12.2	1401	1 LATA_LATMA	P23631 latrodectus
26	162	12.1	656	1 FEM1_CAEEL	P17221 caenorhabdi
27	161	12.0	117	1 MTN_HUMAN	P58546 homo sapien
28	160.5	12.0	452	1 ILK_MOUSE	O55222 mus musculu
29	160.5	12.0	525	1 ASB3_MOUSE	Q9wv72 mus musculu
30	158.5	11.8	347	1 GABG_MOUSE	Q00420 mus musculu
31	158.5	11.8	382	1 GABG_MOUSE	Q00420 mus musculu
32	158.5	11.8	1166	1 TNK2_HUMAN	Q9h2k2 homo sapien
33	157	11.7	775	1 ANR5_MOUSE	Q9d2j7 mus musculu

34	156.5	11.7	347	1 GABG_HUMAN	Q06545 homo sapien
35	156.5	11.7	383	1 GABG_HUMAN	Q06547 homo sapien
36	155	11.6	735	1 RNSA_MOUSE	Q05921 mus musculu
37	154	11.5	777	1 BARI_HUMAN	Q09728 homo sapien
38	153.5	11.4	592	1 V246_FOWPV	Q9j424 fowlpox vir
39	152	11.3	587	1 ASB2_HUMAN	Q96q27 homo sapien
40	151	11.3	768	1 BARI_RAT	Q9qzh2 rattus norv
41	150.5	11.2	168	1 CDN6_HUMAN	P42773 homo sapien
42	149.5	11.1	433	1 ASI4_MOUSE	Q8vhs7 mus musculu
43	149	11.1	227	1 PHLB_SERLI	P18954 serratia 1i
44	149	11.1	323	1 ANKH_CHRVI	O06527 chromatium
45	148.5	11.1	765	1 BARI_MOUSE	O70445 mus musculu

## ALIGNMENTS

RESULT 1  
RFXK\_HUMAN  
ID RFXK\_HUMAN STANDARD; PRT; 260 AA.  
AC O14593; O95839;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE DNA-binding protein RFXANK (Regulatory factor X subunit B) (RFX-B).  
GN RFXANK OR RFXB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND MASS SPECTROMETRY.  
RC TISSUE=B-cell;  
RX MEDLINE=99021383; PubMed=9806546;  
RA Masterak K., Barras E., Zuferey M., Conrad B., Cortals G.,  
RA Aebbersold R., Sanchez J.-C., Hochstrasser D.F., Mach B., Reith W.;  
RT "A gene encoding a novel RFX-associated transactivator is mutated in  
RT the majority of MHC class II deficiency patients.";  
RL Nat. Genet. 20:273-277(1998).  
RN [2]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 79-95; 180-198; 100-210 AND  
RP 238-248.  
RC TISSUE=Lymphoblast;  
RX MEDLINE=99170284; PubMed=10072068;  
RA Nagarajan U.M., Louis-Pence P., Desandro A., Nilsen R., Bushey A.,  
RA Boss J.M.;  
RT "RFX-B is the gene responsible for the most common cause of the bare  
RT lymphocyte syndrome, a MHC class II deficiency.";  
RL Immunity 10:153-162(1999).  
RN [3]  
RP ERRATUM.  
RA Nagarajan U.M., Louis-Pence P., Desandro A., Nilsen R., Bushey A.,  
RA Boss J.M.;  
RL Immunity 10:399-399(1999).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Zhou J., Guan Z., Gu J., Ye M., Fu G., Zhang Q., Xu S., He K.,  
RA Chen S., Mao M., Chen Z.;  
RT "Hematopoiesis-derived ankyrin-like gene.";  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 65-260 FROM N.A.  
RA Lamerdin J.E., McCready P.M., Adamson A.W., Burkhart-Schultz K.,  
RA Christensen M., Gordon L., Kyle A., Ramirez M., Stilwagen S.,  
RA Garnes J., Danganan L., Bruce R., Quan G., Montgomery M., Ow D.,  
RA Kobayashi A., Olsen A.O., Carrano A.V.;  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP VARIANT BLS PRO-195;  
RX MEDLINE=20192025; PubMed=10725724;  
RA Nagarajan U.M., Beijnenburg A., Gobin S.J., Boss J.M.,  
RA van den Elsen P.J.;  
RT "Novel mutations within the RFX-B gene and partial rescue of MHC and

RT related genes through exogenous class II transactivator in  
RT RFX-B-deficient cells."  
RL J. Immunol. 164:3666-3674(2000).  
CC -!- FUNCTION: ACTIVATES TRANSCRIPTION FROM CLASS II MHC PROMOTERS.  
CC ACTIVATION REQUIRES THE ACTIVITY OF THE MHC CLASS II  
CC TRANSACTIVATOR (CIITA). MAY REGULATE OTHER GENES IN THE CELL. RFX  
CC BINDS THE X1 BOX OF MHC-II PROMOTERS. ISOFORM RFX-B-DELTA5 IS NOT  
CC INVOLVED IN THE POSITIVE REGULATION OF MHC CLASS II GENES.  
CC -!- SUBUNIT: RFX CONSISTS OF AT LEAST THREE DIFFERENT SUBUNITS; RFXAP,  
CC RFX5 AND RFX-B/RFXANK; WITH EACH SUBUNIT REPRESENTING A SEPARATE  
CC COMPLEMENTATION GROUP. RFX FORMS COOPERATIVE DNA BINDING COMPLEXES  
CC WITH X2BP AND CBF/NF-Y. RFX ASSOCIATES WITH CIITA TO FORM AN  
CC ACTIVE TRANSCRIPTIONAL COMPLEX.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND  
CC RFX-B-DELTA5; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -!- TISSUE SPECIFICITY: UBIQUITOUS.  
CC -!- DOMAIN: THE THIRD ANKYRIN REPEAT IS REQUIRED FOR ASSOCIATION WITH  
CC THE TWO OTHER RFX SUBUNITS; RFX5 AND RFXAP.  
CC -!- DISEASE: DEFECTS IN RFXANK ARE A CAUSE OF HEREDITARY MHC CLASS II  
CC DEFICIENCY (ALSO KNOWN AS BARE LYMPHOCYTE SYNDROME (BLS) OR HLA  
CC CLASS II-DEFICIENT COMBINED IMMUNODEFICIENCY); A FORM OF SEVERE  
CC COMBINED IMMUNODEFICIENCY DISEASE (SCID). RFXANK IS LINKED WITH  
CC BLS COMPLEMENTATION GROUP B.  
CC -!- SIMILARITY: CONTAINS 5 ANK REPEATS.  
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DR EMBL; AF094760; AAC69883.1; -  
DR EMBL; AF105427; AAD17972.1; -  
DR EMBL; AF105428; AAD17973.1; -  
DR EMBL; AF077196; AAD26991.1; -  
DR EMBL; AC003110; AAB86654.1; -  
DR HSSP; P42773; 1BU9.  
DR Genew; HGNC:9987; RFXANK.  
DR MIM; 603200; -  
DR MIM; 209920; -  
DR InterPro; IPR002110; ANK.  
DR Pfam; PF00023; ank; 4.  
DR SMART; SM00248; ANK; 3.  
DR PROSITE; PS50088; ANK\_REPEAT; 3.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
KW DNA-binding; Transcription regulation; Activator; Nuclear protein;  
KW Repeat; ANK repeat; Alternative splicing; Phosphorylation;  
KW Disease mutation; SCID.  
FT REPEAT 89 118 ANK 1.  
FT REPEAT 123 152 ANK 2.  
FT REPEAT 156 185 ANK 3.  
FT REPEAT 189 218 ANK 4.  
FT REPEAT 222 251 ANK 5.  
FT VARSPLIC 63 63 MISSING (IN ISOFORM RFX-B-DELTA5).  
FT VARSPLIC 91 113 SLISHQLAOGELDQKEHLRKG -> C (IN ISOFORM  
FT VARSPLIC 91 113 RFX-B-DELTA5).  
FT VARIANT 195 195 L->P (IN BLS).  
FT FTid=VAR\_009941.  
SQ SEQUENCE 260 AA; 28102 MW; 6280B490F54816D2 CRC64;

Query Match 100.0%; Score 1341; DB 1; Length 260;  
Best Local Similarity 100.0%; Pred. No. 1.6e-101;  
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MELTOPAEDLIQTQCTPASELGDDEPDGEAADGSDTVLSTLPCTPEPVNPEDASVSS 60  
Db 1 MELTOPAEDLIQTQCTPASELGDDEPDGEAADGSDTVLSTLPCTPEPVNPEDASVSS 60  
Qy 61 PQAGSSLKHSTTLTNRQGENVSALPATLDSLSIHQLAOGELDQKEHLRKGDNLVNKP 120

Db 61 PQAGSSLKHSTTLTNRQGENVSALPATLDSLSIHQLAOGELDQKEHLRKGDNLVNKP 120  
Qy 121 DERGFTPLIWASAFGEIETVRFLLWEGADPHILAKERESALSLASTGTYDIVGLLERD 180  
Db 121 DERGFTPLIWASAFGEIETVRFLLWEGADPHILAKERESALSLASTGTYDIVGLLERD 180  
Qy 181 VDINIYDMNGGTPLLYAVRGNHVKCEVALLARGADLTTEADSGYTPMDLAVALGYRKVOQ 240  
Db 181 VDINIYDMNGGTPLLYAVRGNHVKCEVALLARGADLTTEADSGYTPMDLAVALGYRKVOQ 240  
Qy 241 VIENHILKLFQSNLVPADPE 260  
Db 241 VIENHILKLFQSNLVPADPE 260

RESULT 2  
RFX\_MOUSE STANDARD; PRT; 269 AA.  
ID RFX\_MOUSE  
AC Q9Z205;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE DNA-binding protein RFXANK (Regulatory factor X subunit B) (RFX-B)  
DE (Regulatory factor X-associated ankyrin-containing protein) (Ankyrin  
DE repeat-containing adaptor protein Tvl-1).  
GN RFXANK OR RFXB OR TVL1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Spleen;  
RX MEDLINE=99021383; Pubmed=9806546;  
RA Masteriak K., Barras E., Zuferey M., Conrad B., Corthals G.,  
RA Aebersold R., Sanchez J.C., Hochstrasser D.F., Mach B., Reith W.;  
RT "A gene encoding a novel RFX-associated transactivator is mutated in  
RT the majority of MHC class II deficiency patients."  
RL Nat. Genet. 20:273-277(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=T-cell;  
RX MEDLINE=99262619; Pubmed=10329666;  
RA Lin J.-H., Makris A., McMahon C., Bear S.E., Patriotic C.,  
RA Prasad V.R., Brent R., Golemis E.A., Tschlis P.N.;  
RT "The ankyrin repeat-containing adaptor protein tvl-1 is a novel  
RT substrate and regulator of raf-1."  
RL J. Biol. Chem. 274:14706-14715(1999).  
CC -!- FUNCTION: ACTIVATES TRANSCRIPTION FROM CLASS II MHC PROMOTERS.  
CC ACTIVATION REQUIRES THE ACTIVITY OF THE MHC CLASS II  
CC TRANSACTIVATOR (CIITA). MAY REGULATE OTHER GENES IN THE CELL (BY  
CC SIMILARITY). POTENTIATES THE ACTIVATION OF RAF-1. RFX BINDS THE X1  
CC BOX OF MHC-II PROMOTERS.  
CC -!- SUBUNIT: RFX CONSISTS OF AT LEAST 3 DIFFERENT SUBUNITS; RFXAP,  
CC RFX5 AND RFX-B/RFXANK. RFX FORMS COOPERATIVE DNA BINDING  
CC COMPLEXES WITH X2BP AND CBF/NF-Y. RFX ASSOCIATES WITH CIITA TO  
CC FORM AN ACTIVE TRANSCRIPTIONAL COMPLEX (BY SIMILARITY). FORMS  
CC OLIGOMERS. ASSOCIATES WITH RAF-1.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.  
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A  
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -!- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN THYMUS, LUNG AND  
CC TESTES.  
CC -!- DOMAIN: INTERACTS WITH RAF-1 VIA ITS C-TERMINAL ANKYRIN REPEAT  
CC DOMAIN. THE SAME DOMAIN ALSO MEDIATES ITS HOMODIMERIZATION.  
CC -!- DOMAIN: THE THIRD ANKYRIN REPEAT IS REQUIRED FOR ASSOCIATION WITH  
CC THE TWO OTHER RFX SUBUNITS; RFX5 AND RFXAP (BY SIMILARITY).  
CC -!- PTM: PHOSPHORYLATED BY RAF-1.  
CC -!- SIMILARITY: CONTAINS 3 ANK REPEATS.  
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EMBL; AF094761; AAC69884.1; -  
EMBL; AF123704; AAD24798.1; -  
HSSP; P80144; 2MYO.  
MGD; MGI:1333865; Rfxank.  
InterPro; IPR002110; ANK.  
Pfam; PF00023; ank; 4.  
SMART; SM00248; ANK; 3.  
PROSITE; PS50088; ANK\_REPEAT; 3.  
PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
DNA-binding; Transcription regulation; Activator; Nuclear protein;  
Repeat; ANK repeat; Alternative splicing; Phosphorylation.  
REPEAT 88 127 ANK 1.  
REPEAT 132 161 ANK 2.  
REPEAT 165 194 ANK 3.  
REPEAT 198 227 ANK 4.  
REPEAT 231 260 ANK 5.  
VARSPIC 112 121 MISSING (IN SHORT ISOFORM).  
SEQUENCE 269 AA; 29231 MW; 5713F335DC669E87 CRC64;

Query Match 83.0%; Score 1113.5; DB 1; Length 269;  
Best Local Similarity 81.9%; Pred. No. 4.4e-83;  
Matches 221; Conservative 15; Mismatches 23; Indels 11; Gaps 2;

QY 1 MELTPADLIQTQTPASELGDPEDEADGSDTVVLSLPCTPEVPNPEDASVSS 60  
D 1 MEPTQVAENLVNQPEVPDLEDPEDTRDESPEPNDTVVLSLPCTPDVNPEDASASS 60  
QY 61 PQAGSSLKHSSTLTNRGNEVSALPATLDSLSHQLAQGLDQLKEHLRK----- 112  
D 61 LQ-GSFLKHSSTLTNRGNEVSALPATLDSLSHQLAQGLDQLKEHLRKGCACPACTC 119  
QY 113 --GDNLVNKPDERGFTPLIWASAFGEIETVRFLEWGDPHILAKERESALSTAGYT 170  
D 120 LSGNNLKNKPDGFTPLIWASAFGEIETVRFLEWGDPHILAKERESALSTAGYT 179  
QY 171 DIVGLLEKRDVDINITYDNGGTPPLLYAVRGNHVKVEALLARGADLTTEADSGYTPMDLA 230  
D 180 DIVRLLDKRDVDINITYDNGGTPPLLYAVRGNHVKVEALLARGADLTTEADSGYTPMDLA 239  
QY 231 VALGYRKVQGVTEHNLKLFQSNLVPADPE 260  
D 240 VALGYRKVQGVTEHNLKLFQSNLVPADPE 269

RESULT 3  
ANK2\_HUMAN STANDARD; PRT; 3924 AA.  
ID ANK2\_HUMAN  
AC Q01484; Q01485;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin, nonerythroid).  
GN ANK2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RC TISSUE=Brain stem;  
RX MEDLINE=91302466; PubMed=1830053;  
RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;  
RT "Isolation and characterization of cDNAs encoding human brain  
ankyrins reveal a family of alternatively spliced genes.";  
RL J. Cell Biol. 114:241-253(1991).  
[2]  
RP REVISIONS.  
RA Carpenter S.;

RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Brain stem;  
RX MEDLINE=94075409; PubMed=8253844;  
RA Chan W., Kordeli E., Bennett V.;  
RT "440-kD ankyrinB: structure of the major developmentally regulated  
domain and selective localization in unmyelinated axons.";  
RL J. Cell Biol. 123:1463-1473(1993).  
[4]  
RP SEQUENCE OF 463-495 FROM N.A.  
RX MEDLINE=92009921; PubMed=1833308;  
RA Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,  
RA Lux S.E., Ward D.C., Forget B.G.;  
RT "Isolation and chromosomal localization of a novel nonerythroid  
ankyrin gene.";  
RL Genomics 10:858-866(1991).  
CC -1- FUNCTION: Attach integral membrane proteins to cytoskeletal  
CC elements. Also bind to cytoskeletal proteins.  
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE  
CC PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL  
CC CELLS THROUGHOUT THE BRAIN.  
CC -1- PTM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES  
CC AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE  
CC AND FUNCTION (POTENTIAL).  
CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
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CC -----  
DR EMBL; X56957; CAA40278.1; -.  
DR EMBL; X56958; CAA40279.2; -.  
DR EMBL; Z26634; CAB42644.1; -.  
DR EMBL; M37123; AAA62828.1; -.  
DR PIR; S14533; S14533.  
DR PIR; A39643; A39643.  
DR PIR; B39643; B39643.  
DR PIR; S14569; S14569.  
DR HSSP; P42771; 1DC2.  
DR Genew; HGNC:493; ANK2.  
DR MIM; 106410; -.  
DR InterPro; IPR002110; ANK.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR000906; ZUS.  
DR Pfam; PF00023; ank; 24.  
DR Pfam; PF00531; death; 1.  
DR Pfam; PF00791; ZUS; 1.  
DR PRINTS; PRO1415; ANKYRIN.  
DR SMART; SM00248; ANK; 21.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00218; ZUS; 1.  
DR PROSITE; PS50088; ANK\_REPEAT; 20.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;  
KW Phosphorylation.  
FT REPEAT 63 92 ANK 1.  
FT REPEAT 96 125 ANK 2.  
FT REPEAT 129 158 ANK 3.  
FT REPEAT 162 191 ANK 4.  
FT REPEAT 193 220 ANK 5.  
FT REPEAT 232 261 ANK 6.  
FT REPEAT 265 294 ANK 7.  
FT REPEAT 298 327 ANK 8.  
FT REPEAT 331 360 ANK 9.  
FT REPEAT 364 393 ANK 10.



FT REPEAT 397 426 ANK 11.  
FT REPEAT 430 459 ANK 12.  
FT REPEAT 463 492 ANK 13.  
FT REPEAT 496 525 ANK 14.  
FT REPEAT 529 558 ANK 15.  
FT REPEAT 562 591 ANK 16.  
FT REPEAT 595 624 ANK 17.  
FT REPEAT 628 657 ANK 18.  
FT REPEAT 661 690 ANK 19.  
FT REPEAT 694 723 ANK 20.  
FT REPEAT 727 756 ANK 21.  
FT REPEAT 760 789 ANK 22.  
FT REPEAT 793 822 ANK 23.  
FT DOMAIN 1773 1950 REPEAT-RICH REGION.  
FT REPEAT 1773 1784 REPEAT A.  
FT REPEAT 1785 1796 REPEAT A.  
FT REPEAT 1797 1808 REPEAT A.  
FT REPEAT 1809 1820 REPEAT A.  
FT REPEAT 1821 1832 REPEAT A.  
FT REPEAT 1833 1844 REPEAT A.  
FT REPEAT 1845 1856 REPEAT A.  
FT REPEAT 1857 1867 REPEAT A (APPROXIMATE).  
FT REPEAT 1868 1879 REPEAT A.  
FT REPEAT 1880 1891 REPEAT A.  
FT REPEAT 1892 1902 REPEAT A (APPROXIMATE).  
FT REPEAT 1903 1914 REPEAT A.  
FT REPEAT 1915 1926 REPEAT A.  
FT REPEAT 1927 1938 REPEAT A.  
FT REPEAT 1939 1950 REPEAT A.  
FT DOMAIN 3536 3620 DEATH.  
FT VARSPLIC 1039 1039 O -> QFLGKHLPTAPPPPLNEGESLSVRLQLGPPGTK  
FT VARSPLIC 1444 3528 (IN ISOFORM 2).  
FT CONFLICT 475 476 MISSING (IN ISOFORM 2 AND ISOFORM 3).  
FT CONFLICT 971 971 GO -> PE (IN REF. 4).  
FT CONFLICT 3581 3582 I -> S (IN REF. 1).  
FT CONFLICT 3586 3586 OY -> HA (IN REF. 1).  
SQ SEQUENCE 3924 AA; 430337 MW; 52AC496C428E29D2 CRC64; I -> Y (IN REF. 1).

Query Match 15.1%; Score 202.5; DB 1; Length 3924;  
Best Local Similarity 29.3%; Pred. No. 9.7e-08;  
Matches 56; Conservative 43; Mismatches 81; Indels 11; Gaps 4;

OY 55 DASVSSPQAGSSSLKHSSTLTNRQRGNEVSALPATLDSLSIHQLAOGELDQLKHLRKGD 114  
DB 5 DAAQKS-DSGEKFNSSQRRKPKKSDSNA-----SFLRAAPAGNDKVEYELKGGI 55  
OY 115 NLVKNKPDGFTPLIWSAFGEIETVRFLEWGAADPHILAKERESALSLASTGYTDIVG 174  
DB 56 D-INTCNQGLNALHLAKEGHVLQELLGRGSSVDSATKKGNTALHIASLAGQAEVVK 114  
OY 175 LLLERVDVINYDMNGTGPLLYAVRGNHVKVEALLARGADLTTEADSGYTPMDLAVALG 234  
DB 115 VLKKEGANINAQSQNGFTPLYMAAQENHIDVVKYLLLENGANQSTATEGFTPLAVALQOG 174  
OY 235 YRK-VQOVLEN 244  
DB 175 HNOAVAILLEN 185

RESULT 4

ANK3\_HUMAN STANDARD; PRT; 4377 AA.  
ID ANK3\_HUMAN  
AC Q12955;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ankyrin 3 (ANK-3) (Ankyrin G).  
GN ANK3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;

[1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain stem;  
RX MEDLINE=95138209; Pubmed=7836469;  
RA Kordeli E., Lambert S., Bennett V.;  
RT "Ankyrin. A new ankyrin gene with neural-specific isoforms localized  
at the axonal initial segment and node of Ranvier."  
J. Biol. Chem. 270:2352-2359(1995).  
RL J. Biol. Chem. 270:2352-2359(1995).  
CC -1- FUNCTION: Membrane-cytoskeleton linker.  
CC -1- ALTERNATIVE PRODUCTS: A number of isoforms are produced by  
alternative splicing.  
CC -1- TISSUE SPECIFICITY: Expressed in brain and other tissues.  
CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

-----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; U13616; AAA64834.1; -.  
CC HSSP; P55273; 1B18.  
CC Genew; HGNC:494; ANK3.  
CC MIM; 600465; -.  
CC InterPro; IPR002110; ANK.  
CC InterPro; IPR000488; Death.  
CC InterPro; IPR000906; ZUS.  
CC Pfam; PF00023; ank; 24.  
CC Pfam; PF00531; death; 1.  
CC Pfam; PF00791; ZUS; 1.  
CC PRINTS; PR01415; ANKYRIN.  
CC SMART; SM00248; ANK; 21.  
CC SMART; SM00005; DEATH; 1.  
CC SMART; SM00218; ZUS; 1.  
CC PROSITE; PS50088; ANK\_REPEAT; 21.  
CC PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
CC PROSITE; PS50017; DEATH\_DOMAIN; 1.  
KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat.  
FT REPEAT 73 102 ANK 1.  
FT REPEAT 106 135 ANK 2.  
FT REPEAT 139 168 ANK 3.  
FT REPEAT 172 201 ANK 4.  
FT REPEAT 203 230 ANK 5.  
FT REPEAT 234 263 ANK 6.  
FT REPEAT 267 296 ANK 7.  
FT REPEAT 300 329 ANK 8.  
FT REPEAT 333 362 ANK 9.  
FT REPEAT 366 395 ANK 10.  
FT REPEAT 399 428 ANK 11.  
FT REPEAT 432 461 ANK 12.  
FT REPEAT 465 494 ANK 13.  
FT REPEAT 498 527 ANK 14.  
FT REPEAT 531 560 ANK 15.  
FT REPEAT 564 593 ANK 16.  
FT REPEAT 597 626 ANK 17.  
FT REPEAT 630 659 ANK 18.  
FT REPEAT 663 692 ANK 19.  
FT REPEAT 696 725 ANK 20.  
FT REPEAT 729 758 ANK 21.  
FT REPEAT 762 791 ANK 22.  
FT REPEAT 795 825 ANK 23.  
FT DOMAIN 1519 1898 SER-RICH.  
FT DOMAIN 4090 4174 DEATH.  
SQ SEQUENCE 4377 AA; 480399 MW; F42379E55768B684 CRC64;

Query Match 14.4%; Score 193; DB 1; Length 4377;  
Best Local Similarity 28.1%; Pred. No. 6.7e-07;  
Matches 50; Conservative 43; Mismatches 75; Indels 10; Gaps 3;

OY 68 KHSSTLTNRQRGNEVSALPATLDSLSIHQLAOGELDQLKHLRKGDNLVKNKPDGFTP 127

```
DB 27 KHRKSRDRKKSDANA-----SYLRAPAGHLEKALDYIKNGVD-INICNQGLMA 77
QY 128 LIWASAFGEIETVRFLEWGADPHILAKERESALSLASTGGYTDVIGLLERDVINITYD 187
DB 78 LHLASKEGHEVVESELLQREANVDATKKGNTALHIASLAGQAEVVKVLTNGANVNAQS 137
QY 188 WNGGTPLLAVRGNHVKCVLEALLARGADLTTEADSGYTPMDLVALGY-RKYQQVIEN 244
DB 138 QNGFTPLYMAQENHLEVKFLDNGASQSLATEDGFTPLVALQCGHDQVSLLEN 195

RESULT 5
TNK1_HUMAN
ID TNK1_HUMAN STANDARD; PRT; 1327 AA.
AC 095271; 095272;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tankyrase 1 (EC 2.4.2.30) (TNK1) (Tankyrase I) (TNKS-1) (TRF1-
DE interacting ankyrin-related ADP-ribose polymerase).
GN TNKS OR TNKS1 OR TIN1 OR TIN1L OR PARPL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Testis;
RX MEDLINE=99040105; PubMed=9822378;
RA Smith S., Giriat I., Schmitt A., de Lange T.;
RT "Tankyrase, a poly(ADP-ribose) polymerase at human telomeres.";
RL J. Cell Sci. 112:3649-3656(1999).
RN [2]
RP SUBCELLULAR LOCALIZATION.
RX MEDLINE=99454782; PubMed=10523501;
RA Smith S., de Lange T.;
RT "Cell cycle dependent localization of the telomeric PARP, tankyrase,
RT to nuclear pore complexes and centrosomes.";
RL J. Cell Sci. 112:3649-3656(1999).
RN [3]
RP FUNCTION, AND PHOSPHORYLATION.
RX MEDLINE=20556282; PubMed=10988299;
RA Chi N.-W., Lodish H.F.;
RT "Tankyrase is a golgi-associated mitogen-activated protein kinase
RT substrate that interacts with IRAP in GLUT4 vesicles.";
RL J. Biol. Chem. 275:38437-38444(2000).
RN [4]
RP FUNCTION, AND MUTAGENESIS OF HIS-1184 AND GLU-1291.
RX MEDLINE=21602874; PubMed=11739745;
RA Cook B.D., Dynek J.N., Chang W., Shostak G., Smith S.;
RT "Role for the related poly(ADP-Ribose) polymerases tankyrase 1 and 2
RT at human telomeres.";
RL Mol. Cell. Biol. 22:332-342(2002).
CC -!- FUNCTION: May regulate vesicle trafficking and modulate the
CC subcellular distribution of SLC2A4/GLUT4-vesicles. Has PARP
CC activity and can modify TRF1, and thereby contribute to the
CC regulation of telomere length.
CC -!- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-riboseyl}(N)-acceptor =
CC nicotinamide + {ADP-D-riboseyl}(N+1)-acceptor.
CC -!- SUBUNIT: Oligomerizes and associates with TNKS2. Interacts with
CC the cytoplasmic domain of LNPBP/Otase in SLC2A4/GLUT4-vesicles.
CC Binds to the N-terminus of telomeric TRF1 via the ANK repeats.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and
CC with juxtanuclear SLC2A4/GLUT4-vesicles. A minor proportion is
CC also found at nuclear pore complexes and around the pericentriolar
CC matrix of mitotic centrosomes. During interphase, a small fraction
CC of TNKS is found in the nucleus, associated with TRF1.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
CC produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: Ubiquitous; highest levels in testis.
CC -!- PTM: Upon insulin-stimulation, phosphorylated on serine residues
CC by MAPK kinases.
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CC -!- PTM: ADP-ribosylated (-auto).
CC -!- SIMILARITY: BELONGS TO THE PARP FAMILY.
CC -!- SIMILARITY: CONTAINS 15 ANK REPEATS.
CC -!- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -----
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CC -----
DR EMBL; AF082556; AAC79841.1; -
DR EMBL; AF082557; AAC79842.1; -
DR EMBL; AF082558; AAC79843.1; -
DR EMBL; AF082559; AAC79844.1; -
DR HSSP; Q00420; IAWC.
DR Genew; HGNC:11941; TNKS.
DR MIM; 603303; -.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00023; ank; 21.
DR Pfam; PF00536; SAM; 1.
DR PRINTS; PR01415; ANKRIN.
DR SMART; SM00248; ANK; 15.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS50088; ANK_REPEAT; 15.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50105; SAM_DOMAIN; 1.
DR Transfaser; Glycosyltransferase; NAD; Golgi stack; Telomere;
KW Nuclear protein; Repeat; ANK repeat; ADP-ribosylation;
KW Phosphorylation; Alternative splicing.
FT REPEAT 215 247 ANK 1.
FT REPEAT 248 280 ANK 2.
FT REPEAT 281 313 ANK 3.
FT REPEAT 368 400 ANK 4.
FT REPEAT 401 433 ANK 5.
FT REPEAT 434 466 ANK 6.
FT REPEAT 521 556 ANK 7.
FT REPEAT 557 589 ANK 8.
FT REPEAT 590 622 ANK 9.
FT REPEAT 683 715 ANK 10.
FT REPEAT 716 748 ANK 11.
FT REPEAT 749 781 ANK 12.
FT REPEAT 836 868 ANK 13.
FT REPEAT 869 901 ANK 14.
FT REPEAT 902 934 ANK 15.
FT DOMAIN 1030 1089 SAM.
FT DOMAIN 1176 1327 PARP.
FT DOMAIN 9 14 POLY-HIS.
FT DOMAIN 27 34 POLY-PRO.
FT DOMAIN 128 134 POLY-SER.
FT DOMAIN 137 145 POLY-SER.
FT VARSPLIC 641 643 POLY-SER.
FT VARSPLIC 644 1327 MISSING (IN ISOFORM 2).
FT MUTAGEN 1184 1184 H->A: LOSS OF ACTIVITY; WHEN ASSOCIATED
FT MUTAGEN 1291 1291 WITH A-1291.
FT MUTAGEN 1291 1291 E->A: LOSS OF ACTIVITY; WHEN ASSOCIATED
FT SEQUENCE 1327 AA; 142010 MW; E14DE985C710B957 CRC64;

Query Match 13.9%; Score 187; DB 1; Length 1327;
Best Local Similarity 24.3%; Pred. No. 3.9e-07;
Matches 72; Conservative 36; Mismatches 112; Indels 76; Gaps 9;

QY 18 ASELGDPEDPGEADGSDTV-VLSLPCTPEVPNPEDASVSSPQAGSSLKHSITLTNR 76
DB 137 SSSSSPSSPSSSLAESPEAAGVSTAPLPGAAGP-----GTGVPAVSGALRE---LLEA 189
QY 77 QRGNEVSALPATLDSLSI-----HQLAQGLDQLKHLRKGDNLVKNPDER 123
DB 190 CRNGDVSVRKRLVDAANVANNAKDMAGRKSSPLHFAAGFGRKDVVEHLLOMGAN-VHARDDG 248
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[illegible]

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CC -----
DR EMBL; X16609; CAA34610.1; -.
DR EMBL; M28880; AAA51732.1; -.
DR PIR; S08275; SJHUK.
DR PIR; A35049; A35049.
DR HSSP; Q00420; 1AWC.
DR Genew; HGNC:492; ANK1.
DR MIM; 182900; -.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000488; Death.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00023; ank; 24.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 22.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50088; ANK_REPEAT; 20.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
DR Phosphorylation; Lipoprotein; Disease mutation; Elliptocytosis;
KW Polymorphism.
FT INIT MET 0 0
FT DOMAIN 1 826
FT FT
FT DOMAIN 827 1381
FT FT
FT DOMAIN 1382 1880
FT FT
FT REPEAT 43 72
FT REPEAT 76 105
FT REPEAT 109 138
FT REPEAT 142 171
FT REPEAT 173 200
FT REPEAT 204 233
FT REPEAT 237 266
FT REPEAT 270 299
FT REPEAT 303 332
FT REPEAT 336 365
FT REPEAT 369 398
FT REPEAT 402 431
FT REPEAT 435 464
FT REPEAT 468 497
FT REPEAT 501 530
FT REPEAT 534 563
FT REPEAT 567 596
FT REPEAT 600 629
FT REPEAT 633 662
FT REPEAT 666 695
FT REPEAT 699 728
FT REPEAT 732 761
FT REPEAT 765 794
FT DOMAIN 1402 1486
FT VARSPPLIC 1512 1873
FT VARSPPLIC 1874 1874
FT VARSPPLIC 1849 1880
FT FT
FT FT
FT VARIANT 20 20
FT FT
FT VARIANT 462 462
FT FT
FT VARIANT 618 618
FT FT
FT VARIANT 749 749
FT FT

```

```
FT VARIANT 844 844 D -> E.
FT VARIANT 1285 1285 /FTID=VAR_000599.
FT VARIANT 1391 1391 /FTID=VAR_000601.
FT VARIANT 1591 1591 /FTID=VAR_000600.
FT VARIANT 1698 1698 /FTID=VAR_000602.
FT VARIANT 1698 1698 /FTID=VAR_000603.
FT CONFLICT 229 229 A -> S (IN REF. 2).
FT CONFLICT 1545 1545 V -> I (IN REF. 2).
SQ SEQUENCE 1880 AA; 206145 MW; 1C5F5E7EFD1CD428 CRC64;

Query Match 13.7%; Score 184; DB 1; Length 1880;
Best Local Similarity 23.1%; Pred. No. 1.1e-06;
Matches 54; Conservative 37; Mismatches 69; Indels 74; Gaps 3;

QY 74 TNRQGNVSALPATLDSLSHQLAQGLDQKEHLRKGDNLVNKPDERGFTPLIMASA 133
Db 72 TTTKKN-----TALHIALAGQDEVVRELNVYGAN-VNAQSQKGFPLYMAAQ 119
QY 134 FGEIETVRFLEWGADPHILAKERESALSTGYTDIVG----- 174
Db 120 ENHLEVKFLLNGANQNVATEDGFTPLVALQGHENNVAAHLINYGTKGVRLPALHIA 179
QY 175 -----LLERVDVINIYDWNGG 191
Db 180 ARNDTRTAALLQNDPNPDVLSKGTFTPLHIAHYENLVNQALLNRGASVNFTPQNGI 239
QY 192 TPLLYAVRGNHVKVEALLARGADLTTEADSGYTPMDLAVAGYRKVOQVIENH 245
Db 240 TPLHIASRGNVIMVRLLDGAGQIETKTDELTPHCAARNGHVRISFILLDH 293

RESULT 7
ANK1_MOUSE STANDARD; PRT; 1862 AA.
ID ANK1_MOUSE
AC 002357;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ankyrin 1 (Erythrocyte ankyrin).
GN ANK1 OR ANK-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Erythrocyte;
RX MEDLINE=92345717; PubMed=1386265;
RA White R.A., Birkenmeier C.S., Peters L.L., Barker J.E., Lux S.E.;
RT "Murine erythrocyte ankyrin cDNA: highly conserved regions of the
RT regulatory domain."
RL Mamm. Genome 3:281-285(1992).
CC -!- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
CC ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO
CC NA-K ATPASE, TO THE LYMPOCYTE MEMBRANE PROTEIN GP85, AND TO THE
CC CYTOSKELETAL PROTEINS PODRIN, TUBULIN, VIMENTIN AND DESMIN.
CC ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE
CC CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC
CC PLASMA MEMBRANE.
CC -!- PTM: REGULATED BY PHOSPHORYLATION (BY SIMILARITY).
CC -!- PTM: ACYLATED BY PALMITIC ACID GROUP(S) (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 23 ANK REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC -----
CC EMBL; M84756; AAA37236.1; -.
CC HSSP; Q00420; ANK.
CC MGD; MGI:88024; Ank1.
CC InterPro; IPR002110; ANK.
CC InterPro; IPR000488; Death.
CC Pfam; PF00023; ank; 24.
CC Pfam; PF00531; death; 1.
CC Pfam; PF00791; ZUS; 1.
CC PRINTS; PR01415; ANKYRIN.
CC SMART; SM00248; ANK; 22.
CC SMART; SM00005; DEATH; 1.
CC SMART; SM00218; ZUS; 1.
CC PROSITE; PS50088; ANK_REPEAT; 20.
CC PROSITE; PS50297; ANK_REPEAT_REGION; 1.
CC PROSITE; PS50017; DEATH_DOMAIN; 1.
CC CytoSkelon; Repeat; ANK repeat; Phosphorylation; Lipoprotein.
FT DOMAIN 1 827 89 KDA DOMAIN (ANION EXCHANGE PROTEIN
FT FT 828 1386 BINDING DOMAIN).
FT FT 1387 1862 62 KDA DOMAIN (SPECTRIN BINDING
FT FT 1387 1862 55 KDA REGULATORY DOMAIN (REGULATES
FT FT 1387 1862 THE BINDING OF ANKYRIN TO SPECTRIN
FT FT 1387 1862 AND THE BAND 3 PROTEIN).
FT REPEAT 40 69 ANK 1.
FT REPEAT 73 102 ANK 2.
FT REPEAT 106 135 ANK 3.
FT REPEAT 139 168 ANK 4.
FT REPEAT 170 197 ANK 5.
FT REPEAT 201 230 ANK 6.
FT REPEAT 234 263 ANK 7.
FT REPEAT 267 296 ANK 8.
FT REPEAT 300 329 ANK 9.
FT REPEAT 333 362 ANK 10.
FT REPEAT 366 395 ANK 11.
FT REPEAT 399 428 ANK 12.
FT REPEAT 432 461 ANK 13.
FT REPEAT 465 494 ANK 14.
FT REPEAT 498 527 ANK 15.
FT REPEAT 531 560 ANK 16.
FT REPEAT 564 593 ANK 17.
FT REPEAT 597 626 ANK 18.
FT REPEAT 630 659 ANK 19.
FT REPEAT 663 692 ANK 20.
FT REPEAT 696 725 ANK 21.
FT REPEAT 729 758 ANK 22.
FT REPEAT 762 791 ANK 23.
FT DOMAIN 1399 1483 DEATH.
SQ SEQUENCE 1862 AA; 204242 MW; AE6B85B5B29001E5 CRC64;

Query Match 13.6%; Score 183; DB 1; Length 1862;
Best Local Similarity 23.1%; Pred. No. 1.3e-06;
Matches 54; Conservative 36; Mismatches 70; Indels 74; Gaps 3;

QY 74 TNRQGNVSALPATLDSLSHQLAQGLDQKEHLRKGDNLVNKPDERGFTPLIMASA 133
Db 69 TTTKKN-----TALHIALAGQDEVVRELNVYGAN-VNAQSQKGFPLYMAAQ 116
QY 134 FGEIETVRFLEWGADPHILAKERESALSTGYTDIVG----- 174
Db 117 ENHLEVKFLLNGANQNVATEDGFTPLVALQGHENNVAAHLINYGTKGVRLPALHIA 176
QY 175 -----LLERVDVINIYDWNGG 191
Db 177 ARNDTRTAALLQNDPNPDVLSKGTFTPLHIAHYENLVNQALLNRGASVNFTPQNGI 236
QY 192 TPLLYAVRGNHVKVEALLARGADLTTEADSGYTPMDLAVAGYRKVOQVIENH 245
```



Db 237 TPLHIASTRGVIMVRLLDGAGIETRTKDELTPHCAARNGHVRISEILLDH 290

RESULT 8

PSDA\_MOUSE STANDARD; PRT; 231 AA.

AC Q9Z2X2; Q9D7N8; 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE 26S proteasome non-ATPase regulatory subunit 10 (26S proteasome regulatory subunit p28 (Gankyrin)).

GN PSM10.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RA Higashitsuji H., Fujita J.;

RT "Cloning of mouse gankyrin containing ankyrin repeats.";

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Tongue;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishi Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Wittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S., Hayashizaki Y.;

RA "Functional annotation of a full-length mouse cDNA collection.";

RT Nature 409:685-690(2001).

CC -!- FUNCTION: Acts as a regulatory subunit of the 26S proteasome which is involved in the ATP-dependent degradation of ubiquitinated proteins.

CC -!- SUBUNIT: Component of the PA700 complex.

CC -!- SIMILARITY: CONTAINS 5 ANK REPEATS.

CC -----

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CC -----

DR EMBL; AB022022; BAA36969.1; -

DR EMBL; AK009068; BAB26053.1; -

DR HSSP; P42773; 11HB.

DR MGD; MGI:1858898; Psm10.

DR InterPro; IPR002110; ANK.

DR Pfam; PF00023; ank; 5.

DR PRINTS; PR01415; ANKYRIN.

DR SMART; SM00248; ANK; 5.

DR PROSITE; PS50088; ANK\_REPEAT; 5.

DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.

KW Proteasome; ANK repeat; Repeat.

FT REPEAT 39 68 ANK 1.

FT REPEAT 72 101 ANK 2.

FT REPEAT 105 134 ANK 3.

FT REPEAT 138 167 ANK 4.

FT REPEAT 171 200 ANK 5.

FT CONFLICT 101 101 A -> S (IN REF. 1).

FT CONFLICT 122 122 A -> S (IN REF. 1).

FT CONFLICT 226 226 G -> S (IN REF. 1).

SO SEQUENCE 231 AA; 25053 MW; BCE7B9A79C8CF58B CRC64;

Query Match 13.6%; Score 182.5; DB 1; Length 231;

Best Local Similarity 31.4%; Pred. No. 8e-08;

Matches 54; Conservative 27; Mismatches 86; Indels 5; Gaps 1;

QY 89 LDSLSIHQLAAGELDQLKEHLRKGNLVNKPDERGFTPLMASAFGEIETVRFLEWGA 148

Db 5 VSNIMICNLAYSGLDELKERILADKSLATRTDQDSRTALHWACSGHTEIVEFLQLGV 64

QY 149 DPHILAKERESALSLASTGYTDIVGLLERVDINITYDMNGGTPLLYAVRGNHVCVEA 208

Db 65 PVNDKDDAGWSPLHIAASAGRDEIVKALLVKGAVNAVNGCTPLHYAASKNRHEIAVM 124

QY 209 LLARGADLTTEADSGYTPMDLVALGYRKVQGVIEHILKFSQNLVPADPE 260

Db 125 LLEGANPDADKHYDATAMHRAAKGNLKMV-----HILFFYKASTNIQDTE 171

RESULT 9

YB23\_HUMAN STANDARD; PRT; 768 AA.

AC Q9ULJ7;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical protein KIAA1223 (Fragment).

GN KIAA1223.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=20039619; PubMed=10574462;

RA Nagase T., Ishikawa K.-I., Kikuno R., Hirose M., Nomura N., Ohara O.;

RA "Prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";

RL DNA Res. 6:337-345(1999).

CC -!- SIMILARITY: CONTAINS AT LEAST 14 ANK REPEATS.

CC -----

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CC -----

DR EMBL; AB033049; BAA86537.1; -

DR HSSP; P42771; IDC2.

DR InterPro; IPR002110; ANK.

DR Pfam; PF00023; ank; 14.

DR SMART; SM00248; ANK; 13.

DR PROSITE; PS50088; ANK\_REPEAT; 13.

DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.

KW Hypothetical protein; Repeat; ANK repeat.

FT NON\_TER 1 1

FT REPEAT 1 11 ANK 1.

FT REPEAT 15 44 ANK 2.

FT REPEAT 48 82 ANK 3.

FT REPEAT 86 115 ANK 4.

FT REPEAT 119 148 ANK 5.



FT REPEAT 152 181 ANK 6.  
FT REPEAT 185 214 ANK 7.  
FT REPEAT 218 247 ANK 8.  
FT REPEAT 251 280 ANK 9.  
FT REPEAT 284 313 ANK 10.  
FT REPEAT 317 346 ANK 11.  
FT REPEAT 350 379 ANK 12.  
FT REPEAT 383 412 ANK 13.  
FT REPEAT 416 446 ANK 14.  
SQ SEQUENCE 768 AA; 82819 MW; 2913B69BE2DFE06D CRC64;

Query Match  
Best Local Similarity 13.5%; Score 181.5; DB 1; Length 768;  
Matches 46; Conservative 25; Mismatches 51; Indels 5; Gaps 1;

OY 117 VNKPDGFTPLIWASAFGEIETVRFLLEWGADPHILAKERESALSLA-----STGGYTD 171  
DB 9 VNKADNEGRTALIAAAYMGHREIVEHLLDHGAENVHEDVDGRTALSVAAALCVPAASKGHAS 68  
OY 172 IVGLLERDVIDINIDMNGGTPPLLYAVRGNHVKVEALLARGADLTTEADSGYTPMDLAV 231  
DB 69 VVSLIDRGAEVDHCDKDCMTPLVVAAYEGHVDVVDLLLEGADVDHTDNGRTPLLA 128  
OY 232 ALGYRKV 238  
DB 129 SMGHASV 135

RESULT 10  
PSDA\_HUMAN  
ID PSDA\_HUMAN STANDARD; PRT; 226 AA.  
AC 075832;

DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE 26S proteasome non-ATPase regulatory subunit 10 (26S proteasome regulatory subunit p28) (Gankyrin).  
GN PSMD10.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98382579; PubMed=9714768;  
RA Hori T., Kato S., Saeki M., Demartino G.N., Slaughter C.A., Takeuchi J., Toh-E A., Tanaka K.;  
RT "CDNA cloning and functional analysis of p28 (Nas6p) and p40.5 (Nas7p), two novel regulatory subunits of the 26S proteasome.";  
RL Gene 216:113-122(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RA Higashitsuji H., Fujita J.;  
RT "Enhanced expression of a novel tumour marker in the human hepatomas.";  
RN Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RA Grafham D.;  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Acts as a regulatory subunit of the 26S proteasome which is involved in the ATP-dependent degradation of ubiquitinated proteins.  
CC -!- SUBUNIT: Component of the PA700 complex.  
CC -!- SIMILARITY: CONTAINS 5 ANK REPEATS.  
CC -----  
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DR EMBL; AB009619; BAA33215.1; -.  
DR EMBL; D83197; BAA34594.1; -.  
DR EMBL; AL031177; CAA20117.1; -.  
DR EMBL; BC011960; AAH11960.1; -.  
DR Genew; HGNC:9555; PSMD10.  
DR MIM; 603480; -.  
DR HSSP; P42773; 1IIB.  
DR InterPro; IPR002110; ANK.  
DR Pfam; PF00023; ank; 5.  
DR PRINTS; PR01415; ANKYRIN.  
DR SMART; SM00248; ANK; 5.  
DR PROSITE; PS50088; ANK\_REPEAT; 5.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
KW Proteasome; ANK repeat; Repeat.  
FT REPEAT 39 68 ANK 1.  
FT REPEAT 72 101 ANK 2.  
FT REPEAT 105 134 ANK 3.  
FT REPEAT 138 167 ANK 4.  
FT REPEAT 171 200 ANK 5.  
SQ SEQUENCE 226 AA; 24428 MW; 57158E33146EC7C8 CRC64;

Query Match  
Best Local Similarity 13.2%; Score 176.5; DB 1; Length 226;  
Matches 53; Conservative 28; Mismatches 86; Indels 5; Gaps 1;

OY 89 LDSLSIHQLAOGELDLKELRKDNLVKNPDERGFTPLIWASAFGEIETVRFLLEWGA 148  
DB 5 VSNLMVCNLAVSGLEELKESILADKSLATRTQDSRTALHWACSGHTEIVEFLQLGV 64  
OY 149 DPHILAKERESALSLASTGGYTDIVGLLERDVIDINIDMNGGTPPLLYAVRGNHVKVEA 208  
DB 65 PVNDKDDAGMSPPLHIAASAGRDEIVKALLGKGAOVNAVNGCTPLHYAASKNRHETAVM 124  
OY 209 LLARGADLTTEADSGYTPMDLAVALGYRKYQGVIEHNLKLFQSNLVPADPE 260  
DB 125 LLEGANPDAKDHYEATAMHRAAKGNLKM-----IHLLYYKASTNIQDTE 171

RESULT 11

PSDA\_RAT  
ID PSDA\_RAT STANDARD; PRT; 231 AA.  
AC Q922X3;

DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE 26S proteasome non-ATPase regulatory subunit 10 (26S proteasome regulatory subunit p28) (Gankyrin).  
GN PSMD10.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RA Higashitsuji H., Fujita J.;  
RT "Cloning of rat gankyrin homologue containing ankryrin repeats.";  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Acts as a regulatory subunit of the 26S proteasome which is involved in the ATP-dependent degradation of ubiquitinated proteins.  
CC -!- SUBUNIT: Component of the PA700 complex.  
CC -!- SIMILARITY: CONTAINS 5 ANK REPEATS.  
CC -----  
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RT "Characterization of human skeletal muscle Ankrd2.";  
RL Biochem. Biophys. Res. Commun. 285:378-386(2001).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.  
RX MEDLINE=21347023; PubMed=11453652;  
RA Moriyama M., Tsukamoto Y., Fujiwara M., Kondo G., Nakada C., Baba T.,  
RA Ishiguro N., Miyazaki A., Nakamura K., Hori N., Sato K., Shomori K.,  
RA Takeuchi K., Satoh H., Mori S., Ito H.;  
RT "Identification of a novel human ankyrin-repeated protein homologous  
to CARP.";  
RL Biochem. Biophys. Res. Commun. 285:715-723(2001).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Skeletal muscle;  
RA Strausberg R.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: May play an important role in skeletal muscle  
hypertrophy.  
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be  
produced by alternative splicing.  
CC -!- TISSUE SPECIFICITY: Expressed in skeletal and cardiac muscles.  
CC Found in slow fibers.  
CC -!- SIMILARITY: CONTAINS 5 ANK REPEATS.  
CC -----  
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CC -----  
DR EMBL; AJ304805; CAC19412.1; -  
DR EMBL; AJ304804; CAC19411.1; -  
DR EMBL; AB058599; BAB60958.1; -  
DR EMBL; BC020817; AAH20817.1; -  
DR HSSP; P80144; 2MYO.  
DR Genew; HGNC:495; ANKRD2.  
DR InterPro; IPR002110; ANK.  
DR Pfam; PF00023; ank; 4.  
DR PRINTS; PR01415; ANKYRIN.  
DR SMART; SM00248; ANK; 5.  
DR PROSITE; PS50088; ANK\_REPEAT; 4.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1;  
KW ANK repeat; Repeat; Alternative splicing.  
FT REPEAT 120 149 ANK 1.  
FT REPEAT 153 182 ANK 2.  
FT REPEAT 186 215 ANK 3.  
FT REPEAT 219 248 ANK 4.  
FT REPEAT 252 281 ANK 5.  
FT VARSPLIC 219 251 MISSING (IN ISOFORM 2).  
FT CONFLICT 35 35 T -> A (IN REF. 3).  
SQ SEQUENCE 333 AA; 37151 MW; 679736F0491467A8 CRC64;

Query Match 12.9%; Score 173; DB 1; Length 333;  
Best Local Similarity 32.2%; Pred. No. 7.8e-07;  
Matches 49; Conservative 28; Mismatches 73; Indels 2; Gaps 2;

OY 93 SIHQLAQGELDKHELRKGNLVNKPDERGFTPLIWASAFGELETVRFLLEWGADPHI 152  
DB 157 ALHRASLEGHMEILEKLDNGAT-VDFQDRLDCTAMHWACRGHLEVVKLLQSHGADTNV 215  
OY 153 LAKERESALSLASTGTYTDIVGLLRLRDVDINIDWNGTPLLYAVRGNHVKCVALLAR 212  
DB 216 RDKLSTPLHVAVRTGVEIVHFSLGLEINARDREGDTALHDAVRLNRYKIILLH 275  
OY 213 GADLTTEADSGYTPMDLAVLGYRKVQOVLEN 244  
DB 276 GADMTTKNLAKGKPTDL-VQLWQADTRHALEN 306

ID Y379\_HUMAN STANDARD; PRT; 1059 AA.  
AC O15084;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein KIAA0379 (Fragment).  
GN KIAA0379.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=97349984; PubMed=9205841;  
RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,  
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. VII.  
RT The complete sequences of 100 new cDNA clones from brain which can  
RT code for large proteins in vitro.";  
RL DNA Res. 4:141-150(1997).  
CC -!- SIMILARITY: CONTAINS AT LEAST 27 ANK REPEATS.  
CC -----  
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CC -----  
DR EMBL; AB002377; BAA20833.2; -  
DR HSSP; P80144; 2MYO.  
DR InterPro; IPR002110; ANK.  
DR Pfam; PF00023; ank; 28.  
DR SMART; SM00248; ANK; 26.  
DR PROSITE; PS50088; ANK\_REPEAT; 24.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
KW Hypothetical protein; Repeat; ANK repeat.  
FT NON\_TER 1 1  
FT REPEAT 46 75 ANK 1.  
FT REPEAT 79 108 ANK 2.  
FT REPEAT 112 141 ANK 3.  
FT REPEAT 145 174 ANK 4.  
FT REPEAT 178 207 ANK 5.  
FT REPEAT 211 240 ANK 6.  
FT REPEAT 244 273 ANK 7.  
FT REPEAT 277 307 ANK 8.  
FT REPEAT 311 340 ANK 9.  
FT REPEAT 344 373 ANK 10.  
FT REPEAT 377 406 ANK 11.  
FT REPEAT 410 439 ANK 12.  
FT REPEAT 443 472 ANK 13.  
FT REPEAT 476 506 ANK 14.  
FT REPEAT 510 540 ANK 15.  
FT REPEAT 555 584 ANK 16.  
FT REPEAT 588 617 ANK 17.  
FT REPEAT 622 651 ANK 18.  
FT REPEAT 658 687 ANK 19.  
FT REPEAT 691 720 ANK 20.  
FT REPEAT 724 753 ANK 21.  
FT REPEAT 761 790 ANK 22.  
FT REPEAT 793 823 ANK 23.  
FT REPEAT 828 857 ANK 24.  
FT REPEAT 861 891 ANK 25.  
FT REPEAT 895 924 ANK 26.  
FT REPEAT 931 960 ANK 27.  
SQ SEQUENCE 1059 AA; 113465 MW; C1F55E6CFE494770 CRC64;

Query Match 12.9%; Score 172.5; DB 1; Length 1059;  
Best Local Similarity 22.2%; Pred. NO. 4.3e-06;  
Matches 69; Conservative 43; Mismatches 110; Indels 89; Gaps 9;



QY	22	GDPED-----	EGEEADGSDTVLSLFPCTPEPVNPEPD-----	55
		::	::	
Db	25	GDPEDEVRA LI FKEDVNFQDNEKRTPLHAAAYLGD AEI IELLILSGARVNAKDSKWLTP L		84
QY	56	-----ASVSSPQAGSSLKHSSTLTTLNRCR-----	-----GNEVSALPATLDSIS-----	93
		::	::	
Db	85	HRAVASCSSEAVQVLLKHSADVNARDKNWQTP L HIAANKAVKCAEALVPLLSNVNVS DR		144
QY	94	-----IHQLAAQGLDQLKEHLRKGDNLV NKPDERGFTPLI WASAFGEIETVRFLEWGA		148
		::	::	
Db	145	AGRTALHHAAFSGHGE MVKLLSRGAN-INA FDKDRRAIHWAA YMGHIEVVKLLVSHGA		203
QY	149	DPHILAKERESALSLASTGYTDIVGLLERD VDN-----	-----IYDWNG-----	191
		::	::	
Db	204	EVTCKDKKSYTP L HAAASSGMISVVKYLLDLGYDMNEPNAYGNTPLHVACYNQGDVYVNE		263
QY	192	-----TPLLYAVRGNH-VKCV EALLARGADLTTEADSGYTPMDLAVALG		234
		::	::	
Db	264	LIDCGAIVNQKNNEKGFTPLPHFAA STHGALCIELLVENGADVNMMKSKDGKTP LHMFTALHG		323
QY	235	-YRKVQOV IEN 244		
		::	::	
Db	324	RFSRSQTIITIOS 334		

```

RESULT 15
ILK_CAVPO
ID_ILK_CAVPO      STANDARD;      PRT;      451 AA.
AC      P57044;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Integrin-linked protein kinase (EC 2.7.1.1-) (Beta-integrin-linked
       kinase).
GN      ILK.
OS      Cavia porcellus (Guinea pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
OX      NCBI_TaxID=10141;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Ishii T.;
RL      "Guinea pig beta-integrin-linked kinase.";
       Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC      -|- FUNCTION: RECEPTOR-PROXIMAL, PROTEIN KINASE REGULATING INTEGRIN-
       MEDIATED SIGNAL TRANSDUCTION. MAY ACT AS A MEDIATOR OF INSIDE-OUT
       INTEGRIN SIGNALING. FOCAL ADHESION PROTEIN PART OF THE COMPLEX
       ILK-PINCH. THIS COMPLEX IS CONSIDERED TO BE ONE OF THE CONVERGENCE
       POINTS OF INTEGRIN- AND GROWTH FACTOR-SIGNALING PATHWAY. COULD BE
       IMPLICATED IN MEDIATING CELL ARCHITECTURE, ADHESION TO INTEGRIN
       SUBSTRATES AND ANCHORAGE-DEPENDENT GROWTH IN EPITHELIAL CELLS.
       PHOSPHORYLATES BETA-1 AND BETA-3 INTEGRIN SUBUNIT ON SERINE AND
       THREONINE RESIDUES, BUT ALSO AKT1 AND GSK3B (BY SIMILARITY).
CC      -|- SUBUNIT: INTERACTS WITH CYTOPLASMIC DOMAIN OF BETA 1 SUBUNIT OF
       INTEGRIN. COULD ALSO INTERACTS WITH BETA 2, BETA 3 AND/OR BETA 5
       SUBUNIT OF INTEGRIN. ALSO INTERACTS WITH PINCH AND PARVINS (BY
       similarity).
CC      -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC      -|- DOMAIN: A PH-LIKE DOMAIN IS INVOLVED IN PHOSPHATIDYLINOSITOL
       PHOSPHATE BINDING (BY SIMILARITY).
CC      -|- PTM: AUTOPHOSPHORYLATED ON SERINE (BY SIMILARITY).
CC      -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC      -|- SIMILARITY: CONTAINS 3 ANK REPEATS.
CC      -----
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CC      -----
DR      EMBL; AF256520; AAF70501.1; -.

```

DR	HSSP; Q00420; 1AWC.				
DR	InterPro; IPR002110; ANK.				
DR	InterPro; IPR000719; Euk_pkinase.				
DR	InterPro; IPR002290; Ser_thr_pkinase.				
DR	Pfam; PF00023; ank; 3.				
DR	Pfam; PF00069; pkinase; 1.				
DR	PRINTS; PRO1415; ANKYRIN.				
DR	ProDom; PD000001; Euk_pkinase; 1.				
DR	SMART; SM00248; ANK; 3.				
DR	PROSITE; PS50297; ANK_REPEAT; 1.				
DR	PROSITE; PS50088; ANK_REPEAT; 3.				
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.				
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.				
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.				
KW	Transferase; Serine/threonine-protein kinase; ATP-binding;				
KW	Phosphorylation; Repeat; ANK repeat.				
FT	REPEAT	33	62	ANK 1.	
FT	REPEAT	66	95	ANK 2.	
FT	REPEAT	99	128	ANK 3.	
FT	DOMAIN	180	212	PH-LIKE.	
FT	DOMAIN	193	445	PROTEIN_KINASE.	
FT	NP_BIND	199	207	ATP (BY SIMILARITY).	
FT	BINDING	220	220	ATP (BY SIMILARITY).	
SEQ	SEQUENCE	451 AA;	51308 MW;	88EF22C4517DD52B	CRC64;

Query Match	12.6%;	Score 169.5;	DB 1;	Length 451;
Best Local Similarity	30.4%;	Pred. No. 2.3e-06;		
Matches 48;	Conservative 33;	Mismatches 72;	Indels 5;	Gaps 2;

```

QY      100 QGELDQLEHLRKGDNLVNKEDERGEFTPLIWASAFGEIETVRFLLEMGADPHILAKERES 159
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      10  EGNAAVAVRLWLDNTENDLNQGDHGFSPLHWACREGRSAAVEMTLIMGARLNVMNKGGDT 69

QY      160 ALSLASTGGYTDIVGLLEERDVYNITYDWNNGTPLLAVARGNHVKCVALLARGADLTTE 219
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      70  PLHLASHGHRDIVQKLLQYKADINAVNEHGNVPLHYACFWGQDVAEPLVAN GALVSIC 129

QY      220 ADSGYTPMDLAVALLGYRKVQOVIENHILKLFQS-NLVP 256
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      130 NKYGEMPMDKAKA-----PLRELLRERAEKMGQNLNRIP 163

```

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Search completed: March 17, 2003, 16:40:00
Job time : 15 secs
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